Sample # 1 For GOI from the core + G replacing N determined from reverse sequence:

TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCTGACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTCGATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGCTCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCACCTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACCGCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAGTCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGTAATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTTCTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAAGCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTTCCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCACCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCGGAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTACCTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGTTAACAGTAAAGGTGGATA

Sample # 1 Rev GOI from the core:

TATCCACCTTTACTGTTAACCCAGGAGAACACCACGCATACGGTTAACGGTCGCCTGAGAGATGCCCGCATCACGCAGGTAACCACCCAGAGAACCGTAAGTTTCGTCGATGGTTTGACGAGCCGCTGCCAGGTATTCCGCACGAACACCGAGAACGCCGTCAGACAGACGCGCTTTGGTGAAGGTAACAACCTCCGGTGCCAGTTCGGTGTCGAAACGCTGCTGGATCATTTCAGAGATACGCGCACGCAGTTGCGGAACGCTGTCGTTAGAACGGAGGTAGTCCGCCACAATTACGTCACGATCCAGACCAACCGCTTCCAGAACCAGTGCAACAACGAAGCCGGTACGGTCTTTACCCGCAAAGCAGTGGGTCAGAACCGGACGGCCAGCGGCCAGGAGGGTTACAACACGATGCAGGGCACGCTGCGCACCATTACGGGTCGGGAATTGACGATATTCGTCGGTCATGTAACGAGTGGCTGCATCATTGATAGACTGAGAAGATTCACCAGATTCGCCATTAGAGCCGTCGTTGGTCAGCAGACGTTTGAATGCGGTTTCGTGAGGCGCAGAGTCATCCGCGTCATCGTCCGCGAGATCAGGAAACGGCAGCAGGTGAACGTCGATACCATCTGGAACACGACCTGGACCACGACGAGCAACTTCACGGGAAGAGCGGAGATCGGCAACGTCGGTGATACCCAGACGGCGCANGGTGGCACGACCGGCATCATCGAGACGAGACAGTTCAGAGCTACGGAACAGACGACCCGGACGCAGCGCGGTCGCGGTGTCAGCCACGTCGCGGAAGTTCCACGCACCCGGCAGTTCACGAACCGCCATGGGATTGGAAGTA

GOI:

**TACTTCCAATCC**ATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCTGACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTCGATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGCTCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCACCTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACCGCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAGTCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGTAATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTTCTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAAGCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTTCCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCACCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCGGAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTACCTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGTTAA**CAGTAAAGGTGGATA**

BLAST (subject: S # 1 Rev; query: S # 1 For):

Top of Form

|  | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSB8U1811N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSB8U1811N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSB8U1811N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSB8U1811N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSB8U1811N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) | Links |
| 64251 |  | [1572](http://blast.ncbi.nlm.nih.gov/Blast.cgi#64251) | 1572 | 100% | 0.0 | 99% |  |

Bottom of Form

[Alignments](http://blast.ncbi.nlm.nih.gov/Blast.cgi)

>lcl|64251

Length=859

Score = 1572 bits (851), Expect = 0.0

Identities = 856/859 (99%), Gaps = 1/859 (0%)

Strand=Plus/Minus

Query 1 TACTTCCAAT-CCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGC 59

|||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 859 TACTTCCAATCCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGC 800

Query 60 TGACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCT 119

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 799 TGACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCT 740

Query 120 CGATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCG 179

|||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||

Sbjct 739 CGATGATGCCGGTCGTGCCACCNTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCG 680

Query 180 CTCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCA 239

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 679 CTCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCA 620

Query 240 CCTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAAC 299

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 619 CCTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAAC 560

Query 300 CGCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCA 359

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 559 CGCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCA 500

Query 360 GTCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCG 419

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 499 GTCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCG 440

Query 420 TAATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGT 479

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 439 TAATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGT 380

Query 480 TCTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGA 539

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 379 TCTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGA 320

Query 540 AGCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGT 599

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 319 AGCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGT 260

Query 600 TCCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGC 659

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 259 TCCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGC 200

Query 660 ACCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGC 719

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 199 ACCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGC 140

Query 720 GGAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTA 779

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 139 GGAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTA 80

Query 780 CCTGCGTGATGCGGGCATCTCTCANGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGG 839

|||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||

Sbjct 79 CCTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGG 20

Query 840 TTAACAGTAAAGGTGGATA 858

|||||||||||||||||||

Sbjct 19 TTAACAGTAAAGGTGGATA 1

BLAST (subject: S # 1 For + G replacing N determined from S # 1 Rev; query: GOI):

Top of Form

|  | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSTSNMY11N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSTSNMY11N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSTSNMY11N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSTSNMY11N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=6DSTSNMY11N&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) | Links |
| 1595 |  | [1585](http://blast.ncbi.nlm.nih.gov/Blast.cgi#1595) | 1585 | 100% | 0.0 | 100% |  |

Bottom of Form

[Alignments](http://blast.ncbi.nlm.nih.gov/Blast.cgi)

>lcl|1595

Length=858

Score = 1585 bits (858), Expect = 0.0

Identities = 858/858 (100%), Gaps = 0/858 (0%)

Strand=Plus/Plus

Query 1 TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCT 60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1 TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCT 60

Query 61 GACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTC 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 61 GACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTC 120

Query 121 GATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGC 180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 121 GATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGC 180

Query 181 TCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCAC 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 181 TCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCAC 240

Query 241 CTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACC 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 241 CTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACC 300

Query 301 GCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAG 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 301 GCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAG 360

Query 361 TCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGT 420

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 361 TCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGT 420

Query 421 AATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTT 480

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 421 AATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTT 480

Query 481 CTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAA 540

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 481 CTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAA 540

Query 541 GCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTT 600

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 541 GCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTT 600

Query 601 CCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCA 660

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 601 CCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCA 660

Query 661 CCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCG 720

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 661 CCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCG 720

Query 721 GAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTAC 780

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 721 GAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTAC 780

Query 781 CTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGT 840

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 781 CTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGT 840

Query 841 TAACAGTAAAGGTGGATA 858

||||||||||||||||||

Sbjct 841 TAACAGTAAAGGTGGATA 858